

GenCore version: 4.5
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OM nucleic - nucleic search, using sw model.

Run on: September 17, 2002, 00:04:09 ; Search time 3347.31 Seconds
(without alignments)

11588.820 Million cell updates/sec

Title: US-09-719-017a-2
Perfect score: 1793
Sequence: 1 gaattccctgttgcacaat... caattactcaatggccggcg 1793
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 21979536 seqs, 10817449327 residues
Total number of hits satisfying chosen parameters: 43959072
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_Main:
1: /cgn2_6/ptodata/2/pna/PCRTUS_COMBO.seq: *
2: /cgn2_6/ptodata/2/pna/US0506_COMBO.seq: *
3: /cgn2_6/ptodata/2/pna/US0507_COMBO.seq: *
4: /cgn2_6/ptodata/2/pna/US0801_COMBO.seq: *
5: /cgn2_6/ptodata/2/pna/US0811_COMBO.seq: *
6: /cgn2_6/ptodata/2/pna/US0822_COMBO.seq: *
7: /cgn2_6/ptodata/2/pna/US083_COMBO.seq: *
8: /cgn2_6/ptodata/2/pna/US084_COMBO.seq: *
9: /cgn2_6/ptodata/2/pna/US085_COMBO.seq: *
10: /cgn2_6/ptodata/2/pna/US087_COMBO.seq: *
11: /cgn2_6/ptodata/2/pna/US088_COMBO.seq: *
12: /cgn2_6/ptodata/2/pna/US089_COMBO.seq: *
13: /cgn2_6/ptodata/2/pna/US090_COMBO.seq: *
14: /cgn2_6/ptodata/2/pna/US091_COMBO.seq: *
15: /cgn2_6/ptodata/2/pna/US092_COMBO.seq: *
16: /cgn2_6/ptodata/2/pna/US093_COMBO.seq: *
17: /cgn2_6/ptodata/2/pna/US094_COMBO.seq: *
18: /cgn2_6/ptodata/2/pna/US095_COMBO.seq: *
19: /cgn2_6/ptodata/2/pna/US095A_COMBO.seq: *
20: /cgn2_6/ptodata/2/pna/US095B_COMBO.seq: *
21: /cgn2_6/ptodata/2/pna/US095C_COMBO.seq: *
22: /cgn2_6/ptodata/2/pna/US095D_COMBO.seq: *
23: /cgn2_6/ptodata/2/pna/US096A_COMBO.seq: *
24: /cgn2_6/ptodata/2/pna/US096B_COMBO.seq: *
25: /cgn2_6/ptodata/2/pna/US096C_COMBO.seq: *
26: /cgn2_6/ptodata/2/pna/US096D_COMBO.seq: *
27: /cgn2_6/ptodata/2/pna/US096E_COMBO.seq: *
28: /cgn2_6/ptodata/2/pna/US097A_COMBO.seq: *
29: /cgn2_6/ptodata/2/pna/US097B_COMBO.seq: *
30: /cgn2_6/ptodata/2/pna/US097C_COMBO.seq: *
31: /cgn2_6/ptodata/2/pna/US098_COMBO.seq: *
32: /cgn2_6/ptodata/2/pna/US098B_COMBO.seq: *
33: /cgn2_6/ptodata/2/pna/US098C_COMBO.seq: *
34: /cgn2_6/ptodata/2/pna/US098A_COMBO.seq: *
35: /cgn2_6/ptodata/2/pna/US099B_COMBO.seq: *
36: /cgn2_6/ptodata/2/pna/US099C_COMBO.seq: *
37: /cgn2_6/ptodata/2/pna/US100_COMBO.seq: *
38: /cgn2_6/ptodata/2/pna/US101_COMBO.seq: *
39: /cgn2_6/ptodata/2/pna/US6000_COMBO.seq: *
40: /cgn2_6/ptodata/2/pna/US6001_COMBO.seq: *
41: /cgn2_6/ptodata/2/pna/US6002_COMBO.seq: *
42: /cgn2_6/ptodata/2/pna/US6003_COMBO.seq: *
43: /cgn2_6/ptodata/2/pna/US6004_COMBO.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	954.2	53.2	1071	31 US-09-806-876A-1 Sequence 1, Appli
2	401.6	22.4	7615	15 US-09-108-01-87 Sequence 87, Appli
3	401.6	22.4	7615	19 US-09-502-42-87 Sequence 87, Appli
4	401.6	22.4	7615	19 US-09-502-49-87 Sequence 87, Appli
5	401.6	22.4	7688	15 US-09-108-01-89 Sequence 89, Appli
6	401.6	22.4	7688	19 US-09-502-42-89 Sequence 89, Appli
7	401.6	22.4	7688	19 US-09-502-49-89 Sequence 89, Appli
8	401.6	22.4	7797	15 US-09-108-40-88 Sequence 88, Appli
9	401.6	22.4	7797	19 US-09-502-49-88 Sequence 88, Appli
10	401.6	22.4	7797	19 US-09-502-49-88 Sequence 88, Appli
11	369	20.6	7416	34 US-09-900-57-46 Sequence 46, Appli
12	369	18.7	5641	24 US-09-630-931A-13 Sequence 13, Appli
13	336	18.7	5670	24 US-09-630-931A-14 Sequence 14, Appli
14	336	18.7	5626	24 US-09-630-931A-11 Sequence 11, Appli
15	336	18.7	6043	24 US-09-630-929-4 Sequence 4, Appli
16	336	18.7	6071	24 US-09-630-931A-12 Sequence 12, Appli
17	332.8	18.6	4214	33 US-09-869-696-1 Sequence 1, Appli
18	332.8	18.6	4214	30 US-09-795-872-10 Sequence 10, Appli
19	332.8	18.6	5013	15 US-09-183-188A-5 Sequence 5, Appli
20	332.8	18.6	5013	15 US-09-183-188B-5 Sequence 5, Appli
21	332.8	18.6	5027	1 PCP-US98-27498-6 Sequence 6, Appli
22	332.8	18.6	5027	13 US-08-996-744-6 Sequence 6, Appli
23	332.8	18.6	5069	1 PCP-US98-27498-12 Sequence 12, Appli
24	332.8	18.6	5069	1 PCP-US98-27498-15 Sequence 15, Appli
25	332.8	18.6	5069	13 US-08-996-744-12 Sequence 12, Appli
26	332.8	18.6	5099	1 PCP-US98-27498-15 Sequence 15, Appli
27	332.8	18.6	5099	1 PCP-US98-27498-15 Sequence 15, Appli
28	332.8	18.6	5132	1 PCP-US98-27498-24 Sequence 24, Appli
29	332.8	18.6	5132	13 US-08-996-744-24 Sequence 24, Appli
30	332.8	18.6	5324	1 PCP-US98-27498-31 Sequence 31, Appli
31	332.8	18.6	5324	13 US-08-996-744-31 Sequence 31, Appli

FILE REFERENCE: ELITRA.006A
 CURRENT APPLICATION NUMBER: US/09/630,931A
 PRIOR APPLICATION NUMBER: 60/159, 221
 PRIORITY FILING DATE: 1999-10-13
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 13
 LENGTH: 5641
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 ; OTHER INFORMATION: pJMF3
 ; US-09-630-931A-13

Query Match 18.7%; Score 336; DB 24; Length 5641;
 Best Local Similarity 100.0%; Pred. No. 1.8e-80;
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1441 atgcgcaactcagaagaatcgccgtatggtagtggggctcccatcg 1500
 Qy 1371 agagraggaaacttcggatcaaataacaaaggctcgttgcggcgttt 1430
 Db 1501 agatgttggacttcggatcaaataacaaaggctcgttgcggcgttt 1560
 Qy 1431 tggtttatctgtttttgtcgatggatggatggatggatggatggatgg 1490
 Db 1561 tcgttttatctgtttttgtcgatggatggatggatggatggatggatgg 1620
 Qy 1491 ggatttgaaccttcggatcaaataacaaaggctcgttgcggcgttt 1550
 Db 1621 ggatttgaaccttcggatcaaataacaaaggctcgttgcggcgttt 1680
 Qy 1551 tgccaggatcaaataacaaaggctcgttgcggcgttt 1610
 Db 1681 tgccaggatcaaataacaaaggctcgttgcggcgttt 1740
 Qy 1611 aacttcctctgtcgcatatctacaaggccatcccc 1646
 Db 1741 aacttcctctgtcgcatatctacaaggccatcccc 1776

RESULT 14
 US-09-630-931A-11
 ; Sequence 11, Application US/09630931A
 ; GENERAL INFORMATION:
 ; APPLICANT: Zyskind, Judith W.
 ; TITLE OF INVENTION: CHITOBIASE AS A REPORTER ENZYME
 ; FILE REFERENCE: ELITRA.006A
 ; CURRENT APPLICATION NUMBER: US/09/630,931A
 ; CURRENT FILING DATE: 2000-08-02
 ; PRIOR APPLICATION NUMBER: 60/159, 221
 ; PRIORITY FILING DATE: 1999-10-13
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 11
 LENGTH: 5826
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 ; OTHER INFORMATION: pdYK9
 ; US-09-630-931A-11

Query Match 18.7%; Score 336; DB 24; Length 5826;
 Best Local Similarity 100.0%; Pred. No. 1.8e-80;
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1441 atgcgcaactcagaagaatcgccgtatggtagtggggctcccatcg 1500
 Qy 1371 agatgttggacttcggatcaaataacaaaggctcgttgcggcgttt 1430
 Db 1561 tcgttttatctgtttttgtcgatggatggatggatggatggatgg 1620
 Qy 1491 ggatttgaaccttcggatcaaataacaaaggctcgttgcggcgttt 1550
 Db 1621 ggatttgaaccttcggatcaaataacaaaggctcgttgcggcgttt 1680
 Qy 1551 tgccaggatcaaataacaaaggctcgttgcggcgttt 1610
 Db 1681 tgccaggatcaaataacaaaggctcgttgcggcgttt 1740
 Qy 1611 aacttcctctgtcgcatatctacaaggccatcccc 1646
 Db 1741 aacttcctctgtcgcatatctacaaggccatcccc 1776

Query Match 18.7%; Score 336; DB 24; Length 5670;
 Best Local Similarity 100.0%; Pred. No. 1.8e-80;
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1311 atgcgcaactcagaagaatcgccgtatggtagtggggctcccatcg 1370

RESULT 15
US-09-530-920-4
; Sequence A Application US/09630929
; GENERAL INFORMATION:
; APPLICANT: Judith W. Zyskind
; TITLE OF INVENTION: USE OF EXOENZYME AND SECRETED ENZYMES
; TITLE OF INVENTION: TO MONITOR CELLULAR PROLIFERATION
; FILE REFERENCE: ELITRA.012A
; CURRENT APPLICATION NUMBER: US/09/630,929
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 6043
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Engineered E. coli Plasmid pJFK4 with V. harveyi
; OTHER INFORMATION: sequences inserted
US-09-630-929-4